WHAT IS CLAIMED IS:

1. A method for determining functional links between at least two polypeptides, comprising:

   (a) aligning a primary amino acid sequence of multiple distinct non-homologous polypeptides to the primary amino acid sequences of a plurality of proteins;

   (b) for any alignment found between the primary amino acid sequences of all of such multiple distinct non-homologous polypeptides and the primary amino acid sequence of at least one such protein, outputting an indication identifying the at least one such protein as an indication of a functional link between the multiple polypeptides;

   (c) obtaining data, comprising a list of polypeptides from at least two genomes;

   (d) comparing the list of polypeptides from at least two genomes to form a protein phylogenetic profile for each protein, wherein the protein phylogenetic profile indicates the presence or absence of a polypeptide belonging to a particular protein family in each of the at least two genomes based on homology of the polypeptides; and

   (e) grouping the list of polypeptides from a particular protein family based on similar profiles, wherein a similar profile is indicative of a functional link between the polypeptides;

   (f) comparing the functional links identified in step (b) and step (e) or both to functional links identified by patterns of correlated expression, experimentally measured interactions, and functional relationships.

2. The method of claim 1, further comprising, displaying the functional links as networks of related proteins comprising:

   (g) placing all polypeptides in a diagram such that functionally linked proteins are closer together than all other proteins; and

   (h) identifying proteins that fall in a cluster in said diagram as a functionally related group.